

2115



OIPE

## RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/10/042,417

TIME: 10:06:27

Input Set : A:\5914-090-999.txt

Output Set: N:\CRF3\02112002\J042417.raw

4 <110> APPLICANT: <110 Pagano, M.  
 6 <120> TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF  
 7 PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS  
 9 <130> FILE REFERENCE: 5914-090-999  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/042,417  
 12 <141> CURRENT FILING DATE: 2002-01-07  
 14 <150> PRIOR APPLICATION NUMBER: 60/260,179  
 W--> 15 <151> PRIOR FILING DATE: 2001-01-5  
 17 <160> NUMBER OF SEQ ID NOS: 89  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2151  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
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 29 tcctcagaga gagaagactg taataatggc gaacccccta ggaagataat accagagaag 180  
 30 aattcactta gacagacata caacagctgt gccagactct gcttaaacca agaaacagta 240  
 31 tgttttagcaa gcaactgctat gaagactgag aattgtgtgg ccaaaacaaa acttgccaat 300  
 32 ggcacttcca gtatgattgt gcccaagcaa cggaaactct cagcaagcta tgaaaaggaa 360  
 33 aaggaactgt gtgtcaaata ctttgagcag tggtcagagt cagatcaagt ggaatttgtg 420  
 34 gaacatctta tatcccaaat gtgtcattac caacatgggc acataaactc gtatcttaaa 480  
 35 cctatgttgc agagagattt cataactgct ctgccagctc ggggattgga tcatatcgct 540  
 36 gagaacattc tgtcatacct ggatgccaaa tcaactatgt ctgctgaact tgtgtgcaag 600  
 37 gaatggtacc gactgacctc tgatggcatg ctgtggaaga agcttatcga gagaatggtc 660  
 38 aggacagatt ctctgtggag aggcctggca gaacgaagag gatggggaca gtattttattc 720  
 39 aaaaacaaac ctctgacggg gaatgctcct cccaactctt tttatagagc actttatcct 780  
 40 aaaattatac aagacattga gacaatagaa tctaattgga gatgtggaag acatagttaa 840  
 41 cagagaattc actgccgaag tgaaacaagc aaaggagttt actgtttaca gtatgatgat 900  
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 44 agagtgatca taacaggatc atcggattcc acggtcagag tgtgggatgt aaatacaggt 1080  
 45 gaaatgctaa acacgttgat tcaccattgt gaagcagttc tgcacttgcg tttcaataat 1140  
 46 ggcattgatg tgacctgctc caaagatcgt tccattgctg tatgggatat ggcctcccca 1200  
 47 actgacatta cctcctggag ggtgctggtc ggacaccgag ctgctgtcaa tgtttagtag 1260  
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 50 tacagggaca ggtggtagt gactggctca tctgacaaca ctatcagatt atgggacata 1440  
 51 gaatgtggtg catgtttacg agtggttagaa ggccatgagg aattgggtgcg ttgtattcga 1500  
 52 tttgataaca agaggatagt cagtggggcc tatgatggaa aaattaaagt gtgggatctt 1560  
 53 gtggctgctt tggacccccc tgctcctgca gggacactct gtctacggac ccttgtggag 1620  
 54 cattccggaa gagtttttgc actacagttt gatgaattcc agattgtcag tagttcacat 1680

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See page 5

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56 cgttccccctt ctcgaacata cacctacatc tccagataaa taaccataca ctgacctcat 1800
57 acttgcccag gacccattaa agttgcggtg ttttaacgtat ctgccaatac caggatgagc 1860
58 aacaacagta acaatcaaac tactgcccag tttccctgga ctagccgagg agcagggctt 1920
59 tgagactcct gttgggacac agttggtctg cagtgcggcc aggacggtct actcagcaca 1980
60 actgactgct tcagtgtctg tatcagaaga tgtcttctat caattgtgaa tgattggaac 2040
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67 <213> ORGANISM: Homo sapiens
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74 20 25 30
76 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
77 35 40 45
79 Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
80 50 55 60
82 Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
83 65 70 75 80
85 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
86 85 90 95
88 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
89 100 105 110
91 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
92 115 120 125
94 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
95 130 135 140
97 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
98 145 150 155 160
100 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
101 165 170 175
103 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
104 180 185 190
106 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
107 195 200 205
109 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
110 210 215 220
112 Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
113 225 230 235 240
115 Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
116 245 250 255
118 Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
119 260 265 270
121 Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
122 275 280 285

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124 Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
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128 305                      310                      315                      320
130 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
131                      325                      330                      335
133 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
134                      340                      345                      350
136 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
137                      355                      360                      365
139 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
140                      370                      375                      380
142 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
143 385                      390                      395                      400
145 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
146                      405                      410                      415
148 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
149                      420                      425                      430
151 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
152                      435                      440                      445
154 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
155                      450                      455                      460
157 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
158 465                      470                      475                      480
160 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
161                      485                      490                      495
163 Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
164                      500                      505                      510
166 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
167                      515                      520                      525
169 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
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176                      565
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180 <211> LENGTH: 1476
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 3
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187 ctccagcatc tctccaataa cctagagact ctctcaagc gggacttcct caaactcctt 180
188 cccctggagc tcagttttta tttgttaaaa tggctcgatc ctccagacttt actccatgc 240
189 tgcctcgtct ctaaacagtg gaataagggtg ataagtcgct gtacagaggt gtggcagact 300
190 gcatgtaaaa atttgggctg gcagatagat gattctgttc aggacgcttt gcaactggaag 360
191 aaggttttatt tgaaggttat tttgagaatg aagcaactgg aggaccatga agcctttgaa 420
192 acctcgatcat taattggaca cagtgccaga gtgtatgcac ttactacaa agatggactt 480

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193 ctctgtacag ggtcagatga cttgtctgca aagctgtggg atgtgagcac agggcagtgc 540
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195 acaggctcct ttgacaacac tgtggccttg tgggaatgga gttccggagc caggacccag 660
196 cactttcggg ggcacacggg ggcggtatgt agcgtggact acaatgatga actggatatc 720
197 ttggtgagcg gctctgcaga cttcactgtg aaagtatggg ctttatctgc tgggacatgc 780
198 ctgaacacac tcaccgggca cacggaatgg gtcaccaagg tagttttgca gaagtgcaaa 840
199 gtcaagtctc tcttgcacag tcctggagac tacatcctct taagtgcaga caaatatgag 900
200 attaagattt ggccaattgg gagagaaatc aactgtaagt gcttaaagac attgtctgtc 960
201 tctgaggata gaagtatctg cctgcagcca agacttcatt ttgatggcaa atacattgtc 1020
202 tgtagttcag cacttggctc ctaccagtg gactttgccca gttatgatat tctcagggtc 1080
203 atcaagactc ctgagatagc aaacttggcc ttgcttggct ttggagatat ctttgccctg 1140
204 ctgtttgaca accgctacct gtacatcatg gacttgcgga cagagagcct gattagtgcg 1200
205 tggcctctgc cagagtacag ggaatcaaag agaggctcaa gcttcctggc aggcgaacat 1260
206 cctggctgaa tggactggat gggcacaatg acacgggctt ggtctttgcc accagcatgc 1320
207 ctgaccacag tattcacctg gtgttggtga aggagcacgg ctgacaccat gagccaccac 1380
208 cgctgactga ctttgggtgc cggggctgcg ggttttgggt gcacctctgc ggcacgcgac 1440
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211 &lt;210&gt; SEQ ID NO: 4

212 &lt;211&gt; LENGTH: 422

213 &lt;212&gt; TYPE: PRT

214 &lt;213&gt; ORGANISM: Homo sapiens

216 &lt;400&gt; SEQUENCE: 4

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221           20           25           30
223 Ile Ser Leu Ser Gly Ala Val Gln Leu Arg His Leu Ser Asn Asn Leu
224           35           40           45
226 Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
227           50           55           60
229 Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr Cys
230           65           70           75           80
232 Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu
233           85           90           95
235 Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp Ser
236           100          105          110
238 Val Gln Asp Ala Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile Leu
239           115          120          125
241 Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser Leu
242           130          135          140
244 Ile Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly Leu
245           145          150          155          160
247 Leu Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp Val Ser
248           165          170          175
250 Thr Gly Gln Cys Val Tyr Gly Ile Gln Thr His Thr Cys Ala Ala Val
251           180          185          190
253 Lys Phe Asp Glu Gln Lys Leu Val Thr Gly Ser Phe Asp Asn Thr Val
254           195          200          205
256 Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg Gly

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263      245      250      255
265 Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val Thr
266      260      265      270
268 Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser Pro
269      275      280      285
271 Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile Trp
272      290      295      300
274 Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser Val
275 305      310      315      320
277 Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp Gly
278      325      330      335
280 Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp Phe
281      340      345      350
283 Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Ile Ala Asn
284      355      360      365
286 Leu Ala Leu Leu Gly Phe Gly Asp Ile Phe Ala Leu Leu Phe Asp Asn
287      370      375      380
289 Arg Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser Arg
290 385      390      395      400
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300 <211> LENGTH: 1407
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302 <213> ORGANISM: Homo sapiens
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307 atgagcattc tcagacttgt gattggggta atctccttca ggacattatt ctccaagtat 180
308 ttaaataattt gcctcttctt gaccgggctc atgcttcaca agtttgccgc aactggaacc 240
309 aggtatttca catgcctgac ttgtggagat gttttgaatt tgaactgaat cagccagcta 300
310 catcttattt gaaagctacc catccagagc tgatcaaaca gattattaaa agacattcaa 360
311 accatctaca atatgtcagc ttcaagggtg acagcagcaa ggaatcagct gaagcagctt 420
312 gtgatatact atcgcaactt gtgaattgct ctttaaaaaa acttggaact atttcaactg 480
313 ctcgaccaag ctttatggat ttaccaaagt ctcaacttat ctctgcactg acagtttgtt 540
314 tcgtaaaactc caaatccctg tcttcgctta agatagatga tactccagta gatgatccat 600
315 ctctcaaagt actagtggcc aacaatagtg atacactcaa gctgttgaaa atgagcagct 660
316 gtctcatgtt ctctccagca ggtatccttt gtgtggctga tcagtgtcac ggcttaagag 720
317 aactagccct gaactaccac ttattgagtg atgattgtgt acttgcattg tcttctgaaa 780
318 aacatgttcg attagaacat ttgcgcattg atgtagttag tgagaatcct ggacagacac 840
319 acttccatac tattcagaag agtagctggg atgctttcat cagacattca cccaaagtga 900
320 acttagtgat gtattttttt ttatatgaag aagaatttga ccccttcttt cgctatgaaa 960
321 tacctgccac ccattctgtac tttgggagat cagtaagcaa agatgtgctt ggccgtgtgg 1020

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:1262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
L:2541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51  
L:2660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52  
L:2663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52  
L:2683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53  
L:2746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:2776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:2782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:2788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:3079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59